

Amendments to the Claims

This listing of claims will replace all prior versions and listings of claims in the application:

Claims 1-32 (cancelled)

33. (New) A method for generating a secondary library of protein variants of a target protein comprising:

- a) inputting the coordinates of said target protein into a computer;
- b) utilizing a scoring function to generate a filtered set of optimized primary variant sequences filtered for desired properties;
- c) generating a list of primary variant positions in said primary variant sequences;
- d) combining a plurality of said primary variant positions to generate a secondary library of secondary sequences; and
- e) synthesizing a plurality of secondary sequences.

34. (New) A method according to claim 33 wherein said combining comprises:

- a) generating a set of oligonucleotide probes each encoding at least one of said variant amino acid residues;
- b) using said probes in a polymerase chain reaction (PCR) to generate a plurality of oligonucleotide sequences, each encoding at least one of said secondary variant proteins; and,
- c) producing said secondary variant proteins in host cells transformed with said oligonucleotide sequences.

35. (New) A method according to claim 33, wherein said scoring function is selected from the group consisting of a van der Waals potential scoring function, a hydrogen bond potential scoring function, an atomic solvation scoring function, an electrostatic scoring function and a secondary structure propensity scoring function.

36. (New) A method according to claim 33 wherein said step b) utilizes Protein Design Automation to computationally generate said optimized primary variant sequences.

37. (New) A method according to claim 33 wherein said generating of said primary variant positions is by using a probability distribution table.

38. (New) A method according to claim 33 wherein said combining of said primary variant positions is by using a probability distribution table.

39. (New) A method according to claim 33 wherein said combining is done computationally.

40. (New) A method according to claim 33 wherein said combining and synthesizing are done simultaneously using gene shuffling.

41. (New) A method according to claim 33 wherein said combining and synthesizing are done simultaneously using multiple PCR with pooled oligonucleotides.